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0 20 40
GAAAATGGCGCCTCACGGCCC GG TAGTCTTACGACCCTGGTGCCCTGGCTGCCGCCCT
-----+-----+-----+-----+-----+-----+-----
CTTTTACCGCGGAGTGCCGGGCCATCAGAATGCTGGGACCA CGGGACCCGACGGCGGGA
M A P H G P G S L T T L V P W A A A L

60 80 100
GCTCCTCGCTCTGGCGTGGAAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCC
-----+-----+-----+-----+-----+-----+-----
CGAGGAGCGAGACCCGACCTTCCGAGACC CGCGATGGGCTCTACGTGGTTACAGG
L L A L G V E R A L A L P E I C T Q C P

120 140 160
AGGGAGCGTGCAAAATTGTCAAAAGTGGCCTTTATTGTAAAACGACACGAGAGCTAAT
-----+-----+-----+-----+-----+-----+-----
TCCCTCGCACGTTAACAGTTCA CCGGAAATAACATTTGCTGTGCTCTCGATTA
G S V Q N L S K V A F Y C K T T R E L M

180 200 220
GCTGCATGCCCGTTGCTGCCTGAATCAGAAGGGCACCATCTGGGGCTGGATCTCCAGAA
-----+-----+-----+-----+-----+-----+-----
CGACGTACGGGCAACGACGGACTTAGTCTTCCGTGGTAGAACCCGACCTAGAGGTCTT
L H A R C C L N Q K G T I L G L D L Q N

240 260 280
CTGTTCTCTGGAGGACCTGGTCAAACCTTCATCAGGCACATACCACTGTCA TCAGA
-----+-----+-----+-----+-----+-----+-----
GACAAGAGACCTCCTGGGACCAGGTTGAAAGTAGTCCGTATGGTGACAGTAGTATCT
C S L E D P G P N F H Q A H T T V I I D

300 320 340
CCTGCAAGCAAACCCCTCAAAGGTGACTTGGCCAACACCTCCGTGGTTACTCAGCT
-----+-----+-----+-----+-----+-----+-----
GGACGTTCGTTGGGGAGTTCCACTGAACCGGGTGTGGAAAGGCACCGAAATGAGTCGA
L Q A N P L K G D L A N T F R G F T Q L

FIG. 1A

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360

380

400

CCAGACTCTGATACTGCCACAAACATGTCAACTGTCTGGAGGAATTAAATGCCTGGAATAC
---+-----+-----+-----+-----+-----+
GGTCTGAGACTATGACGGTGTGTACAGTTGACAGGGACCTCCTTAATTACGGACCTTATG
Q T L I L P Q H V N C P G G I N A W N T

420

440

460

TATCACCTCTTATATAGACAACCAAATCTGTCAAGGGAAAAGAACCTTGCAATAACAC
---+-----+-----+-----+-----+-----+
ATAGTGGAGAATATATCTGTTGGTTAGACAGTCCCCGTTCTGGAAACGTTATTGTG
I T S Y I D N Q I C Q G Q K N L C N N T

480

500

520

TGGGGACCCAGAAATGTGTCCTGAGAATGGATCTTGTGTACCTGATGGTCCAGGTCTTT
---+-----+-----+-----+-----+-----+
ACCCCTGGGTCTTACACAGGACTCTTACCTAGAACACATGGACTACCAGGTCCAGAAAA
G D P E M C P E N G S C V P D G P G L L

540

560

580

GCAGTGTGTTGTGCTGATGGTTCCATGGATACAAGTGTATGCCGCCAGGGCTCGTTCTC
---+-----+-----+-----+-----+-----+
CGTCACACAAACACGACTACCAAAGGTACCTATGTTCACATACGCGGTCCCGAGCAAGAG
Q C V C A D G F H G Y K C M R Q G S F S

600

620

640

ACTGCTTATGTTCTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTTG
---+-----+-----+-----+-----+-----+
TGACGAATAACAAGAAGCCCTAACGACCCCTCGGTGGTAGAGATAGGCAGAGGTAAGACGAAAC
L L M F F G I L G A T T L S V S I L L W

660

680

700

GGCGACCCAGCGCCGAAAAGCCAAGACTCATGAACATAGGTCTTACCATGGACCTA
---+-----+-----+-----+-----+-----+
CCGCTGGGTCGCGGCTTTCGGTCTGAAGTACTGATGTATCCAGAATGGTAACGGAT
A T Q R R K A K T S *

FIG. 1B

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720 740 760
AGATCAATCTGAACTATCTTAGCCCAGTCAGGGAGCTCTGCTCCTAGAAAGGCATCTT
---+-----+-----+-----+-----+-----+-----
TCTAGTTAGACTTGATAGAATCGGGTCAGTCCCTCGAGACGAAGGATCTTCCGTAGAAA

780 800 820
CGCCAGTGGATTGCCTCAAGGTTGAGGCCATTGGAAGATGAAAAATTGCACTCCCT
---+-----+-----+-----+-----+-----+-----
GCGGTACCTAACGGAGTTCCAACCTCCGGCGGTAAACTTCTACTTTAACGTGAGGGA

840 860 880
TGGTGTAGACAAATACCAGTTCCATTGGTGTGCTATAATAAACACTTTTCTT
---+-----+-----+-----+-----+-----+-----+-----
ACCACATCTGTTATGGTCAAGGGTAACCACAACGGATATTATTGTGAAAAAGAA

900
TTTAAAAAAAAAAAAAAA
---+-----+-----
AAAATTTTTTTTTTTTTTT

FIG. 1C

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Human TGF α VVSHFNDCPDSHTQF-CFH-GTCRFLVQEDKPACVCHSGYVGARCEHADLIA
 | | | | |
 GQKNLCNNNTGDPREMCPENGSCVPDGPGLLQ-cVCADGFHGYKCMRQGSFSLIM

TGF α -III

FIG. 2